22

cD2-996

100

## APPENDIX\_A

## PRIMERS DESIGNED FOR DEN-2 CLONING/SEQUENCING PROJECT:

SEQ.	•		
ID NO:	PRIMER	MER/SENSE	SROURNCR
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3	PUC/H13-P5	25/+	5'-CCCAGTCACGACGTTGTAAAACCAC-3'
4	PUC/M13-P5B	27/+	5'-GGATGTGCTGCAAGGCCATTAAGTTGG-3'
5	POC/HT3-53	25/+	5'-TGAGCGGATAACAATTTCACACAGG-3'
6	PUC/H13-P3B	27/-	5'-GGCTTTACACTTTATGCTTCCGGCTCG-3'
7	D2-1-ECO.T7 75/+		5'-GCGGATATTG/GAATTC/TCTAGA/ AATTTAATACGACTCACTATA/ AGTTGTTAGTCTACGTGGACCGACAAAGACAG-3'
			(5'-Fill /RcoRI /XbaI/T7 Promoter/ 5'-end of DEN-2)
8	D2-SMT71	77/+	5'-ccagt/gaattc/gagctc/acgcgt/ aaatttaatacgactcactata/ agttgttggtctacgtggaccgacaaagacag-3'
			(5'-Pill/EcoRI/SstI/MluI/T7 Promoter/ 5'-end of DEN-2)
9	D2-1	24/+	5'-AGTTGTTAGTCTACGTGGACCGAC-3'
10	D2-28	34/+	5'-GACAGATTCTT MGAGGGAGCTGAGCTCAACUTAG-3'
11	D2-134	28/+	5'-TCAATATGCTGAAACGCDAGAGAAACCG-3'
12	cD2-250 .	26/-	5'-GGGATTGTTAGGAAACGAAGGAACGC-3'
13 .	D2-274	32/+	5'-CCACCAACAGCAGGGATACTGAAAAGATGGGG-3'
14	cD2-378	25/-	5'-TGCAGATCTGCGTCTCCTATTCAAG-3'
15	D2-528	25/+	5'-CGTGAACATGTGTACCCTCATGGCC-3'
16	cD2-616	26/-	5'-TTGCACCAACAGTCAATGTCTTCAGG-3'
17	D2-616	25/+	5'-ACCAGAGACATAGATTGTTGGTGC-3'
18	cD2-618	25/-	5'-GCACCAACAGTCTATGTCTTCTGGC-3'
19	cD2-771	25/-	5'-ATGITICCAGGCCCCTICTGATGAC-3'
20	D2-847	25/+	5'-GCAGCAATCCTGGCATACACCATAG-3'
21	D2-996	27/+	5'-GGTTGACATAGTCTTAGAACATGGAAG-3'

5'-CITCCATGITCTAAGACTATGTCAACC-3'

SEQ.			101
MO:	PRIMER	MER/SENSE	SROUBNCR
23 .	.D2-1005	35/+	5'-GTCTTALIAACATGGAAGTTGTGTGACGACGATGGC-3'
24	D2-1141	25/+	5'-ACAACAGAATCTCGCTGCCCAACAC-3'
25	D2-1211	25/+	5'-GCAAACACTCCATGGTAGACAGAGG-3'
26	cD2-1211	25/-	5'-CCTCTGTCTACCATGGAGTGTT10C-3'
27	CD2-1227	27/-	5'-CCACATCCATTTCCCCATCCTCTOTCT-3'
28	D2-1261	30/+	5'-GGAAAGGGAGGCATTGTGACCTGTGCTATG-3'
29	D2-1416	28/+	5'-GGAAATCAAAATAACACCACAGAGTTCC-3'
30	cD2-1503	34/-	5'-CTGCAGCAACACCATCTCATTGAAGTCGACGCCC-3'
31	D2-1510	25/+	5'-GACTTCAATGAGATGGTGCTGCT3'
32	cD2-1510	25/+	5'-GCAGCAGCACCATCTCATTGAAGTC-3'
33	D2-1546	28/+	5 - AAGCTTGGCTGGTGCACAGGCAATGGTT-3
34	cD2-1567	27/-	5 - TGGTAACGGCAGGTCTAGGAACCATTG-3
35	D2-1777	23/+ -	5'-GGACATCTCAAGTGCAGGCTGAG-3'
36	cD2-1777	23/+	5'-CTCAGCCTGCACTTGAGATGTCC-3'
37	D2-1863	27/+	5'-GAAGGAAATAGCAGAAACACAACATCG-3'
38	CD2-1986	33/-	5'-CCCTTCATATTGTACTCTQATAACTATTGTTCC-3'
39	D2-2047	32/+	5'-CCTCCATTCGGAGACAGCTACATCATCATAGG-3'
40	cD2-2047	32/-	5'-CCTATGATGATGTAGCTGTCTCCGAATGGAGG-3'
41	D2-2170	29/+	5'-ATGGCCATTTIAGGTGALACAGCCTGGGA-3'
42	cD2-2200	27/ -	5'-TGTAAACACTCCTCCCAGGGATCCAAA-3'
43	D2-2308	29/+	5'-CTCATAGGAGTCATTATCACATGGATAGG-3'
44	cD2-2504	35/-	5'-GGGGATTCTGGTTGGAACTTATATTGTTCTGTCC-3'
45	eD2-2622	30/-	5'-TGATTCAATTCTGGTGTTATTTGTTTCCAC-3'
46	D2-2702	25/+	5'-AAGGAATCATGCAGGCAGGAAAACG-3'
47	cD2-2864	22/-	5'-ACTTCCAGCGAGTTCCAAGCTC-3' A A
48	D2-2992	25/+	5'-AACAGAGCCGTCCATGCCGATATGG-3'
49	cD2-3105	22/-	5'-TCCATTGCTCCABAGGGTGTGT-3'
50	D2-3236	25/+	5'-AGCTTGAGATGGACTTTGATTTCTG-3'

SEQ. ID			102
NO:	PRIMER	MER/SENSE	SEODERCE
51	cD2-3410	22/-	5'-GGTCTGATTTCCATCCCGTACC-3'
52	D2-3621	23/+	5'-GTCCTTTAGAGACCTGGGAAGAG-3'
53	cD2-3739	25/-	5'-GTTTTCTCAAGAGTAGTCCAGCTGC-3' C
54	D2-3905	25/+	5'-ATCAATIGGCAGTGACTATCATGGC-3'
55	cD2-4002	25/-	5'-TGTTANGAGCAGTGGAGAAACGGAC-3' A G
56	cD2-4060 .	25/-	5'-GATTUAGACCTTTGATCGTCAACGC-3'
57	D2-4214	25/+	5'-TGACAGGACCATTAGTGGCTGGAGG-3'
58	112-4257	34/+	5'-OFFICETCACTGGACGATCGGCCGATTTGGAACTG-3'
59	cD2-4323	24/-	5'-GGGCTGCTTCCTGATATTTCTGCC-3'
60	D2-4497	25/+	5'-CCTUTGGGAAGTGAAGAAACAACGG-3'
61	cD2-4557	30/	5'-GCTCCATCTTCCAGTTCAGCCTTTCCCATG-3'
62 .	cD2-4615	25/-	G G A
63	D2-4746	25/+	5'-CCTAATATCATATGGAGGAGGCTGG-3'
64	D2-4792	25/+	5'-GRAGGAGAAGAAGTCCAGGTATTGG-3'
65	cD2-4922	25/-	5'-CTOTOGACANTTGGAGATCCTGACG-3' T T
66	D2-4994	25/+	5'-GTGGAGCATATGTGAGTGCTATAGC-3'
67	D2-5124	25/+	5'-TCTGACTATGGCCGGAAGGTATCTC-3'
68	D2-5173	-25/+	5'-ACATTAATCTTGGCCCCCCACTAGAG-3'
69	CD2-5272	19/-	5'-GGATCTCCCGCCCGGTGTG-3' A
70	cD2-5318	25/	5'-CTAACTGGTGATAGCAGCCTCATGG-3'
71 .	cD2-5656	27/-	5'-CCTACTGAGTTGTATCACTTTCTTTCC-3'
72	cD2-5891	26/-	5'-TGGATTTCTTCCTATTCTCCCTCTTC-3'
73	D2-5770	25/+	5'-TTCARGGCTGAGAGGGTTATAGACC-3'
74	D2-6152	25/+	5'-TCTGGFTGGCCTACAGAGTGGCAGC-3'
75	cD2-6252	27/-	5'-CCTTCTTTTGTCCAGATTTCCACTTCC-3' A

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SEQ.			103
ID No:	PRIMER	MER/SENSE	SKOULVICK
***************************************			MAYMANICH
76	D2-6493	35/+	5'-GCGTACAACCATGCTCTCAGTGAACTGCCCGAGAC-3'
77	cD2-6605	24/-	5'-TTCCCAGGGTCATCTTCCCTAIAC-3'
78	cD2-6624	31/-	5'-GATGCTAGCOGTGATTATGCAGCACATTCCC-3'
79	D2-6748	25/+	5'-AAACAGAGAACACCCCAAGACAACC-3'
80	cD2-6932	21/-	5'-OGGCATACAGCGTCCATGCTG-3'
81	D2-7055	25/+	5'-GTCTCGGGAAAGGATGGCCATTGTC-3'
82	cD2-7195	25/-	5'-CTCTGGTTGCTTTTGCTTGAAGTCC-3'  G G
83	cD2-7217	27/-	5'-COGCOGCTGCTCTTTTCTGAGCTTCTC-3'
84	D2-7378	25/+	5'-AGGACTACATGGGCTCTGTGTGAGG-3'
85	cD2-7515	19/-	5'-GAGAAGTCCAGCTCCGGCC-3'
86	D2-7769	25/+	5'-AGAGAAACATGGTCACACCAGAAGG-3'
87	cD2-7885	22/-	5'-GTTCTTOGTGTCCTGGTCCTCC-3'
88 .	D2-8165	25/+	5'-GGAAATATGGAGGAGCCTAGTGAGG-3'
89	cD2-8210	22/-	5'-ACCCAGIACATCTCATGIGIGG-3'
90	D2-8429	28/+	5'-GAGCATGAAACATCATGGCACTATGACC-3'
91	D2-8440	25/+	5'-TCATGGCACTATGACCAAGACCACC-3'
92	cD2-8529	22/-	5'-CAGTCTGACCACTCCGTTCACC-3' C A G
93	D2-8773	25/+	5'-AAGGTGAGAAGCAATGCAGCCTTGG-3'
94	D2-B798	29/+	5'-GGGCCATATTCACTGATGAGAACAAGTGG-3'
95	cD2-8865	22/-	5'-TCTTTCCCTGTCAACCAGCTCC-3' C T
96	D2-9046	25/+	5'-AATGAAGATCACTGGTTCTCCAGAG-3'
97	D2-9131	25/+	5'-ACCTGAGCAAGAAAGAGGGAGGAGC-3'
98	cD2-9166	22/-	5.1-TGTCCCATCCTGCTGTGTCATC-3* A G
99	cD2-9234	30/-	5'-GCTAGTTTCTTGTGTTCTCCTTCCATGTGG-3'
100	D2-9344 ·	25/+	5'-TCATATCGAGAAGAGACCAAAGAGG-3'
101	cD2-9429	24/-	5'-ACTCCTTCTCCCTCCATCTGTCTO-3'

SEQ.			104
15Q1_	PRIMER	MER/SENSE	SROUBICE
102	cD2-9438	<b>27/</b> -	5'-ATGCTTTTGAAGATTCCTTCTCCCCCC-3' A C
103	CD2-9468	32/-	5'-GCACAGOGATTTCTTCTGTGATTGTTAGGTGC-3'
104	D2-9645	25/+	5'-ACAATGGGAACCTTCAAGAGGATGG-3'
105	D2-9656.BAM	45/+	5'-TTATCACATT/GGATCC/TTCAAGAGGATGGA ATGATTGGACACAAG-3''
			(5'-Fill/BamHI/DEN-2 Sequence)
106	cD2-9668	28/-	5'-CAGAAGGGCACTTGTGTCCAATCATTCC-3
107	cD2-9779	21/-	5'-CTCCCTGGGAAATTCGGGCTC-3' T G
108	cD2-9796	. 28/-	5'-COGTCTCCCGCAAAGACCACCCTGCTCC-3'
109	cD2-9796 XBA	44/-	5'-TTATCACCTA/TCTAGA/CCGTCTCCC3'
110	cD2-9913	26/-	5'-GTTGGAACCCAATGTGATGGTACTGC-3'
111	D2-9937	25/+	5'-ACAGTCGAACAACCTGGTCCATAC-3'
112	cD2-9977	21/-	5'-GCATGTCTTCCGTQGTCATCC-3' T
113	cD2-10003	25/-	5'-CTTGAATCCACACCCTGTTCCAGAC-3'
114	D2-10203	25/+	5'-ATACACAGATTACATGCCATCCATG-3'
115	cD2-10261	21/-	5'-TTTTGCCTTCTACCACAGGAC-3' T A
116	D2-10289	25/-	5'-GAAACAAGGCTAGAAGTCAGGTCGG-3'
117	cD2-10337	23/-	5'-GACGGGGCTCACAGGTAGCATAG-3'
118	D2-10418	25/.+	5'-GCCTGTAGCTCCACCTGAGAAGGTG-3'
119	D2-10470	25/+	5'-GGAAGCTGTACGCATGGCGTAGTGG-3'
120	cD2-10530	19/-	5'-GGGCCCCCGTTGTTGCTGC-3'
121	cD2-10687	59/-	5'-AGAACCTGTTGATTCAACAGCACCATTCCATTTTCTG-3'
122	eD2-10687.XBA	<b>59/-</b>	5'-TTATCACCTA/GCATGC/TCTAGA/ AGAACCTGTTGATTCAACAGCACCATTCCATTTTCTG-3'
-			(5'-Fill/SphI/XbaI/ 3'-Bnd DEN-2 Sequence)
123	cD2-10687.X2	<b>52/</b> .	5'-TTATCACCTA/TCTAGA/ GAACCTGTTGATTCAACAGCACCATTCCATTTTCTG-3'

(5'-Fill/MbaI/ 3'-End DEN-2 Sequence)